# **Filter out Short Sequences**

To use this workflow input a set of sequences and set a minimum sequence length. All sequences with length less than the specified value will be filtered out. The result will be written into a FASTA file by default.

## How to Use This Sample

If you haven't used the workflow samples in UGENE before, look at the "How to Use Sample Workflows" section of the documentation.

### Workflow Sample Location

The workflow sample "Filter out Short Sequences" can be found in the "Scenarios" section of the Workflow Designer samples.

### Workflow Image

The opened workflow looks as follows:

| Read        | Sequence | Length Marker    | Output<br>data | Filter             | filtered-<br>data | Write Long         |
|-------------|----------|------------------|----------------|--------------------|-------------------|--------------------|
| Sequence    | 0        |                  | 5              |                    | 5                 | Sequences          |
|             |          | Identifies an    |                | Filters input data |                   |                    |
| Reads       |          | input seaquence  |                | from Length        |                   | Save all sequences |
| sequence(s) |          | as long or short |                | Marker by          |                   | from Read Sequence |
| from unset. |          |                  |                | value(s) long.     |                   | to default file.   |

#### Workflow Wizard

The wizard has 3 pages.

1. Input sequence(s): On this page, input files must be set.

| • Filter short sequences |                   | 8             |
|--------------------------|-------------------|---------------|
|                          | Input sequence(s) |               |
|                          | Dataset 1 🔯       | ÷             |
|                          | ▶ 😂 🔒 🔨 ↓ 😣       |               |
|                          |                   |               |
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| VII                      |                   |               |
| UGENE                    |                   |               |
| Defaults                 |                   | Next > Cancel |
| Deraults                 |                   | Next > Cancel |

2. Filtering: The filtering parameters can be changed here.

| Filter short sequences |   |                                      | 8 |
|------------------------|---|--------------------------------------|---|
| J                      | Filtering                                   |                                      |   |
|                        | Sequence Length Threshold<br>Minimum length | 10000                                |   |
|                        |   | [10000                               |   |
|                        |   |                                      |   |
|                        |   |                                      |   |
|                        |   |                                      |   |
|                        |   |                                      |   |
|                        |   |                                      |   |
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|                        |   |                                      |   |
| UGENE                  | c.  |                                      |   |
| Defaults               | (   | < <u>B</u> ack <u>N</u> ext > Cancel |   |

The following parameters are available:

Minimum length Minimum sequence length

3. <u>Output data:</u> On this page, the output file can be selected:

| • Filter short sequences |                            | 6                    | 8 |
|--------------------------|----------------------------|----------------------|---|
|                          | Output data                |                      |   |
|                          | Output data<br>Result file |                      |   |
| Defaults                 | < <u>B</u> a               | ack Apply Run Cancel |   |